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         SEP 27
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- L2 ANSWER 4 OF 4 MEDLINE on STN
- AN 2000455673 MEDLINE
- DN PubMed ID: 10966650
- TI The orientation of DNA in an archaeal transcription initiation complex.
- CM Comment in: Nat Struct Biol. 2000 Sep;7(9):703-5. PubMed ID: 10966630
- AU Bartlett M S; Thomm M; Geiduschek E P
- CS Department of Biology and Center for Molecular Genetics, University of California, San Diego, La Jolla, California 92093-0634, USA.. bartlett@biomail.ucsd.edu
- SO Nature structural biology, (2000 Sep) 7 (9) 782-5. Journal code: 9421566. ISSN: 1072-8368.
- CY United States
- DT Journal; Article; (JOURNAL ARTICLE)
- LA English
- FS Priority Journals; Space Life Sciences
- EM 200009
- ED Entered STN: 20001005

Last Updated on STN: 20001005 Entered Medline: 20000928

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- L2 ANSWER 1 OF 4 CA COPYRIGHT 2004 ACS on STN
- RNA polymerase from the hyperthermophile archaeon Pyrococcus furiosus AΒ (Pfu) forms specific and transcriptionally active complexes with its conjugate transcription factors TBP (the archaeal TATA binding protein homolog) and TFB (the archaeal homolog of eukaryotic RNA polymerase II and III transcription factors TFIIB and Brf) at the Pfu glutamate dehydrogenase promoter. A photochem. crosslinking method was used to map vicinity of the catalytic subunits of Pfu RNA polymerase to DNA locations distributed along the polymerase-promoter interface. component of this archaeal polymerase is split into two subunits, A' and A'', whose relatively sharp boundary of DNA crosslinking (probed on the transcribed strand) is centered five to six base pairs downstream of the transcriptional start site. A strong argument based on this information, on the well-defined homol. between the core bacterial, archaeal and eukaryotic RNA polymerase subunits, and on the recently determined structure of a bacterial RNA polymerase specifies the directionality of DNA in the archaeal transcription complex and its trajectory downstream of the transcriptional start site.
- AN 134:142663 CA
- TI The orientation of DNA in an archaeal transcription initiation complex
- AU Bartlett, Michael S.; Thomm, Michael; Geiduschek, E. Peter
- CS Department of Biology and Center for Molecular Genetics, University of California, La Jolla, CA, 92093-0634, USA
- SO Nature Structural Biology (2000), 7(9), 782-785 CODEN: NSBIEW; ISSN: 1072-8368
 - PB Nature America Inc.
 - DT Journal
 - LA English
 - RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT
 - L2 ANSWER 2 OF 4 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN Deamination of cytosine to uracil in a G-C base pair is a major promutagenic event, generating G-CfwdarwA-T mutations if not repaired before DNA replication. Archaeal family B DNA polymerases are uniquely able to recognize unrepaired uracil in a template strand and stall polymerization upstream of the lesion, thereby preventing the irreversible fixation of an A-T mutation. We have now identified a 'pocket' in the N-terminal domains of archaeal DNA polymerases that is positioned to interact with the template strand and provide this ability. The structure

of this pocket provides interacting groups that discriminate uracil from the four normal DNA bases (including thymine). These groups are conserved in archaeal polymerase but absent from homologous viral polymerases that are unable to recognize uracil. Using site-directed mutagenesis, we have confirmed the biological role of this pocket and have engineered specific mutations in the Pfu polymerase that confer the ability to read through template-strand uracils and carry out PCR with dUTP in place of dTTP.

- AN 2003:81516 BIOSIS
- DN PREV200300081516
- TI Structural basis for uracil recognition by archaeal family B DNA polymerases.
- AU Fogg, Mark J.; Pearl, Laurence H.; Connolly, Bernard A. [Reprint Author]
- CS School of Cell and Molecular Biosciences, University of Newcastle, Newcastle upon Tyne, NE2 4HH, UK b.a.connolly@ncl.ac.uk
- SO Nature Structural Biology, (December 2002) Vol. 9, No. 12, pp. 922-927. print.
 ISSN: 1072-8368 (ISSN print).
- DT Article
- LA English
- ED Entered STN: 6 Feb 2003 Last Updated on STN: 6 Feb 2003
- L2 ANSWER 3 OF 4 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN RNA polymerase from the hyperthermophile archaeon Pyrococcus furiosus AΒ (Pfu) forms specific and transcriptionally active complexes with its conjugate transcription factors TBP (the archaeal TATA binding protein homolog) and TFB (the archaeal homolog of eukaryotic RNA polymerase II and III transcription factors TFIIB and Brf) at the Pfu qlutamate dehydrogenase promoter. A photochemical crosslinking method was used to map the vicinity of the catalytic subunits of Pfu RNA polymerase to DNA locations distributed along the polymerase-promoter interface. largest component of this archaeal polymerase is split into two subunits, A' and A", whose relatively sharp boundary of DNA crosslinking (probed on the transcribed strand) is centered five to six base pairs downstream of the transcriptional start site. A strong argument based on this information, on the well-defined homology between the core bacterial, archaeal and eukaryotic RNA polymerase subunits, and on the recently determined structure of a bacterial RNA polymerase specifies the directionality of DNA in the archaeal transcription complex and its trajectory downstream of the transcriptional start site.
- AN 2000:490391 BIOSIS
- DN PREV200000490512
- TI The orientation of DNA in an archaeal transcription initiation complex.
- AU Bartlett, Michael S. [Reprint author]; Thomm, Michael; Geiduschek, E. Peter
- CS Department of Biology and Center for Molecular Genetics, University of California, San Diego, La Jolla, CA, 92093-0634, USA
- SO Nature Structural Biology, (September, 2000) Vol. 7, No. 9, pp. 782-785. print.
 ISSN: 1072-8368.
- DT Article
- LA English
- ED Entered STN: 15 Nov 2000 Last Updated on STN: 10 Jan 2002
- L2 ANSWER 4 OF 4 MEDLINE on STN
- AB RNA polymerase from the hyperthermophile archaeon Pyrococcus furiosus (Pfu) forms specific and transcriptionally active complexes with its conjugate transcription factors TBP (the archaeal TATA binding protein homolog) and TFB (the archaeal homolog of eukaryotic RNA polymerase II and III transcription factors TFIIB and Brf) at the Pfu glutamate dehydrogenase promoter. A photochemical crosslinking method was used to

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- CS Department of Biology and Center for Molecular Genetics, University of California, San Diego, La Jolla, California 92093-0634, USA.. bartlett@biomail.ucsd.edu
- SO Nature structural biology, (2000 Sep) 7 (9) 782-5. Journal code: 9421566. ISSN: 1072-8368.
- CY United States
- DT Journal; Article; (JOURNAL ARTICLE)
- LA English
- FS Priority Journals; Space Life Sciences
- EM 200009
- ED Entered STN: 20001005

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FILE 'CA, BIOSIS, MEDLINE' ENTERED AT 16:53:55 ON 17 NOV 2004 694 S POLY U SEPHAROSE?

L2 4 S ARCHAEAL POLYMERASE

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